

SEQUENCE LISTING

<110> Godfrey, Wayne
Buck, David
Engleman, Edgar G.

<120> Receptor on the Surface of Activated T-Cells: ACT-4

<130> 16524.010

<150> US 08/472,940

<151> 1995-06-06

<150> US 08/147,784

<151> 1993-11-03

<160> 2

<210> 1

<211> 1058

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (15)..(845)

<220>

<223> ACT-4-h-1 cDNA

<400> 1

cagcagagac	gagg	atg	tgc	gtg	ggg	gct	cgg	cgg	ctg	ggc	cgc	ggg	cgc	50
		Met	Cys	Val	Gly	Ala	Arg	Arg	Leu	Gly	Arg	Gly	Pro	
		1				5					10			
tgt	gcg	gct	ctg	ctc	ctc	ctg	ggc	ctg	ggg	ctg	agc	acc	gtg	98
Cys	Ala	Ala	Leu	Leu	Leu	Leu	Gly	Leu	Gly	Leu	Ser	Thr	Val	
	15					20					25			
ctc	cac	tgt	gtc	ggg	gac	acc	tac	ccc	agc	aac	gac	cgg	tgc	146
Leu	His	Cys	Val	Gly	Asp	Thr	Tyr	Pro	Ser	Asn	Asp	Arg	Cys	
	30					35					40			
gag	tgc	agg	cca	ggc	aac	ggg	atg	gtg	agc	cgc	tgc	agc	cgc	194
Glu	Cys	Arg	Pro	Gly	Asn	Gly	Met	Val	Ser	Arg	Cys	Ser	Arg	
	45				50					55				60
aac	acg	gtg	tgc	cgt	ccg	tgc	ggg	ccg	ggc	ttc	tac	aac	gac	242
Asn	Thr	Val	Cys	Arg	Pro	Cys	Gly	Pro	Gly	Phe	Tyr	Asn	Asp	
			65						70				75	
agc	tcc	aag	ccg	tgc	aag	ccc	tgc	acg	tgg	tgt	aac	ctc	aga	290
Ser	Ser	Lys	Pro	Cys	Lys	Pro	Cys	Thr	Trp	Cys	Asn	Leu	Arg	
		80						85				90		
agt	gag	cgg	aag	cag	ctg	tgc	acg	gcc	aca	cag	gac	aca	gtc	338

0985245-051101

Ser	Glu	Arg	Lys	Gln	Leu	Cys	Thr	Ala	Thr	Gln	Asp	Thr	Val	Cys	Arg	
	95						100					105				
tgc	cgg	gcg	ggc	acc	cag	ccc	ctg	gac	agc	tac	aag	cct	gga	gtt	gac	386
Cys	Arg	Ala	Gly	Thr	Gln	Pro	Leu	Asp	Ser	Tyr	Lys	Pro	Gly	Val	Asp	
	110					115					120					
tgt	gcc	ccc	tgc	cct	cca	ggg	cac	ttc	ttc	cca	ggc	gac	aac	cag	gcc	434
Cys	Ala	Pro	Cys	Pro	Pro	Gly	His	Phe	Ser	Pro	Gly	Asp	Asn	Gln	Ala	
	125				130					135					140	
tgc	aag	ccc	tgg	acc	aac	tgc	acc	ttg	gct	ggg	aag	cac	acc	ctg	cag	482
Cys	Lys	Pro	Trp	Thr	Asn	Cys	Thr	Leu	Ala	Gly	Lys	His	Thr	Leu	Gln	
				145					150					155		
ccg	gcc	agc	aat	agc	tgc	gac	gca	atc	tgt	gag	gac	agg	gac	ccc	cca	530
Pro	Ala	Ser	Asn	Ser	Ser	Asp	Ala	Ile	Cys	Glu	Asp	Arg	Asp	Pro	Pro	
			160					165					170			
gcc	acg	cag	ccc	cag	gag	acc	cag	ggc	ccc	ccg	gcc	agg	ccc	atc	act	578
Ala	Thr	Gln	Pro	Gln	Glu	Thr	Gln	Gly	Pro	Pro	Ala	Arg	Pro	Ile	Thr	
		175					180					185				
gtc	cag	ccc	act	gaa	gcc	tgg	ccc	aga	acc	tca	cag	gga	ccc	tcc	acc	626
Val	Gln	Pro	Thr	Glu	Ala	Trp	Pro	Arg	Thr	Ser	Gln	Gly	Pro	Ser	Thr	
	190					195					200					
cgg	ccc	gtg	gag	gtc	ccc	ggg	ggc	cgt	gcg	gtt	gcc	gcc	atc	ctg	ggc	674
Arg	Pro	Val	Glu	Val	Pro	Gly	Gly	Arg	Ala	Val	Ala	Ala	Ile	Leu	Gly	
	205				210					215				220		
ctg	ggc	ctg	gtg	ctg	ggg	ctg	ctg	ggc	ccc	ctg	gcc	atc	ctg	ctg	gcc	722
Leu	Gly	Leu	Val	Leu	Gly	Leu	Leu	Gly	Pro	Leu	Ala	Ile	Leu	Leu	Ala	
				225					230					235		
ctg	tac	ctg	ctc	cgg	agg	gac	cag	agg	ctg	ccc	ccc	gat	gcc	cac	aag	770
Leu	Tyr	Leu	Leu	Arg	Arg	Asp	Gln	Arg	Leu	Pro	Pro	Asp	Ala	His	Lys	
			240				245						250			
ccc	cct	ggg	gga	ggc	agt	ttc	cgg	acc	ccc	atc	caa	gag	gag	cag	gcc	818
Pro	Pro	Gly	Gly	Gly	Ser	Phe	Arg	Thr	Pro	Ile	Gln	Glu	Glu	Gln	Ala	
	255					260					265					
gac	gcc	cac	tcc	acc	ctg	gcc	aag	atc	tgac	cttg	ggc	ccacca	aggt			866
Asp	Ala	His	Ser	Thr	Leu	Ala	Lys	Ile								
	270					275										
ggacgctggg	ccccgccagg	ctggagcccg	gagggctctgc	tgggcgagca	gggcaggtgc											926
aggccgcctg	ccccgccacg	ctcctgggcc	aactctgcac	cgttctaggt	gccgatggct											986
gcctccggt	ctctgcttac	gtatgccatg	catacctcct	gccccgcggg	accacaataa											1046
aaaccttggc	ag															1058

<211> 277
<212> PRT
<213> Homo sapiens

<220>
<223> deduced amino acid sequence of ACT-4-h-1

<400> 2

Met Cys Val Gly Ala Arg Arg Leu Gly Arg Gly Pro Cys Ala Ala Leu
1 5 10 15
Leu Leu Leu Gly Leu Gly Leu Ser Thr Val Thr Gly Leu His Cys Val
20 25 30
Gly Asp Thr Tyr Pro Ser Asn Asp Arg Cys Cys His Glu Cys Arg Pro
35 40 45
Gly Asn Gly Met Val Ser Arg Cys Ser Arg Ser Gln Asn Thr Val Cys
50 55 60
Arg Pro Cys Gly Pro Gly Phe Tyr Asn Asp Val Val Ser Ser Lys Pro
65 70 75 80
Cys Lys Pro Cys Thr Trp Cys Asn Leu Arg Ser Gly Ser Glu Arg Lys
85 90 95
Gln Leu Cys Thr Ala Thr Gln Asp Thr Val Cys Arg Cys Arg Ala Gly
100 105 110
Thr Gln Pro Leu Asp Ser Tyr Lys Pro Gly Val Asp Cys Ala Pro Cys
115 120 125
Pro Pro Gly His Phe Ser Pro Gly Asp Asn Gln Ala Cys Lys Pro Trp
130 135 140
Thr Asn Cys Thr Leu Ala Gly Lys His Thr Leu Gln Pro Ala Ser Asn
145 150 155 160
Ser Ser Asp Ala Ile Cys Glu Asp Arg Asp Pro Pro Ala Thr Gln Pro
165 170 175
Gln Glu Thr Gln Gly Pro Pro Ala Arg Pro Ile Thr Val Gln Pro Thr
180 185 190
Glu Ala Trp Pro Arg Thr Ser Gln Gly Pro Ser Thr Arg Pro Val Glu
195 200 205
Val Pro Gly Gly Arg Ala Val Ala Ala Ile Leu Gly Leu Gly Leu Val
210 215 220
Leu Gly Leu Leu Gly Pro Leu Ala Ile Leu Leu Ala Leu Tyr Leu Leu
225 230 235 240
Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly
245 250 255

0985245.051101

Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser
260 265 270

Thr Leu Ala Lys Ile
275

09852845-051101